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 CCCCCCT
 CACAGACTACCGCTCTCACT

PubMed

Nucleotide

Protein

Genome

Structure

PopSet

Taxonomy

OMIM

Boo

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☐ 1: Z35595. *Caenorhabditis el...*[gi:3217055]

Links

LOCUS CEC01G6 2049 bp DNA linear INV 12-NOV-2002
 DEFINITION *Caenorhabditis elegans* cosmid C01G6, complete sequence.
 ACCESSION Z35595 REGION:
 join(29625..29756,29826..29976,30144..30261,30306..30571,
 30689..30931,31048..31295,31342..31522,31806..32115,32165..32257,
 32307..32533,32582..32661)
 VERSION Z35595.1 GI:3217055
 KEYWORDS HTG; 4-coumarate-coA ligase; Glycerol facilitator protein; Kringle
 domain; MIP; NADPH-ferrihemoprotein reductase; Protein tyrosine
 receptor ror1; Zinc finger (C3HC4 type).
 SOURCE *Caenorhabditis elegans*
 ORGANISM *Caenorhabditis elegans*
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 Rhabditoidea; Rhabditidae; Peloderinae; *Caenorhabditis*.
 REFERENCE 1
 AUTHORS none.
 TITLE Genome sequence of the nematode *C. elegans*: a platform for
 investigating biology. The *C. elegans* Sequencing Consortium
 JOURNAL Science 282 (5396), 2012-2018 (1998)
 MEDLINE 99069613
 REMARK The *C.elegans* Sequencing Consortium.
 REFERENCE 2 (bases 1 to 2049)
 AUTHORS Berks,M.
 TITLE Direct Submission
 JOURNAL Submitted (02-AUG-1994) Nematode Sequencing Project, Sanger
 Institute, Hinxton, Cambridge CB10 1SA, England and Department of
 Genetics, Washington University, St. Louis, MO 63110, USA. E-mail:
 jes@sanger.ac.uk or rw@nematode.wustl.edu
 COMMENT On Jun 13, 1998 this sequence version replaced gi:521002.
 Coding sequences below are predicted from computer analysis, using
 predictions from Genefinder (P. Green, U. Washington), and other
 available information.
 Current sequence finishing criteria for the *C. elegans* genome
 sequencing consortium are that all bases are either sequenced
 unambiguously on both strands, or on a single strand with both a
 dye primer and dye terminator reaction, from distinct subclones.
 Exceptions are indicated by an explicit note.
 IMPORTANT: This sequence is not the entire insert of clone C01G6.
 It may be shorter because we only sequence overlapping sections
 once, or longer because we arrange for a small overlap between
 neighbouring submissions.
 The true left end of clone C01G6 is at 1 in this sequence. The true
 right end of clone C01G6 is at 42193 in this sequence. The true
 left end of clone D2013 is at 43257 in this sequence. The start of
 this sequence (1..104) overlaps with the end of sequence AL021147.
 The end of this sequence (43257..43410) overlaps with the start of
 sequence Z47808.

For a graphical representation of this sequence and its analysis see:- <http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?name=C01G6>

IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

FEATURES Location/Qualifiers

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 CDS 1..2049
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 Score=59.7, E-value=1.2e-15, N=1
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BASE COUNT 646 a 397 c 447 g 559 t
ORIGIN

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Revised: July 5, 2002.

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Dec 5 2002 18:17:57